

ABSTRACT OF THE DISCLOSURE

The invention relates to methods for the elucidation of a transcriptional profile of a cell and for methods to facilitate functional genome annotation. The method of this invention relies on random integration of an artificial exon or a nucleotide fragment that tags the RNA of the gene into which it integrates. In eukaryotic cells, it allows the simultaneous identification of exon-intron boundaries for genome annotation. The gene trapping based strategy for transcript tagging is followed by recovery of those tags fused to flanking cellular exon sequences. Polymerization of those tags allows for high-throughput sequencing and characterization of exon-intron boundaries. Moreover, determination of the frequencies of each particular tag is used to determine the relative transcriptional level of each tagged RNA variant.